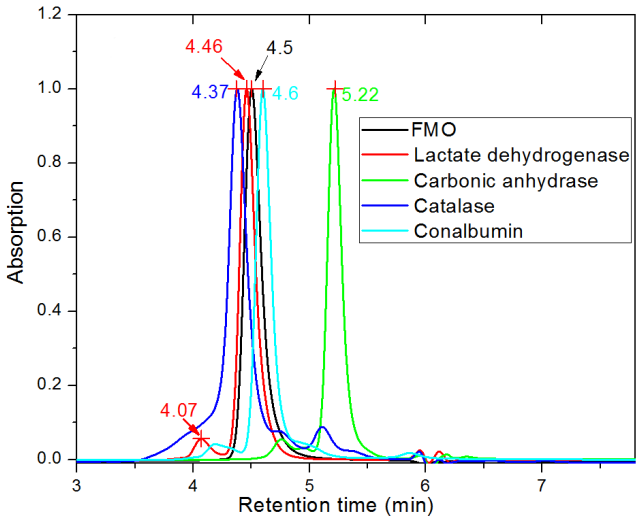
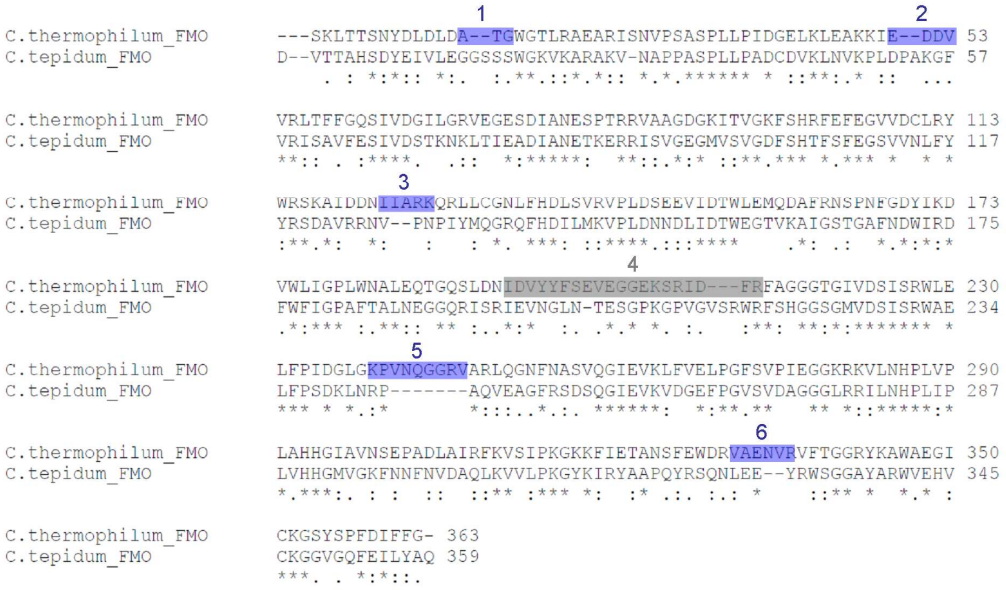
Supplemental information

Structural model and spectroscopic characteristics of the FMO antenna protein from the aerobic chlorophototroph, *Candidatus* Chloracidobacterium thermophilum

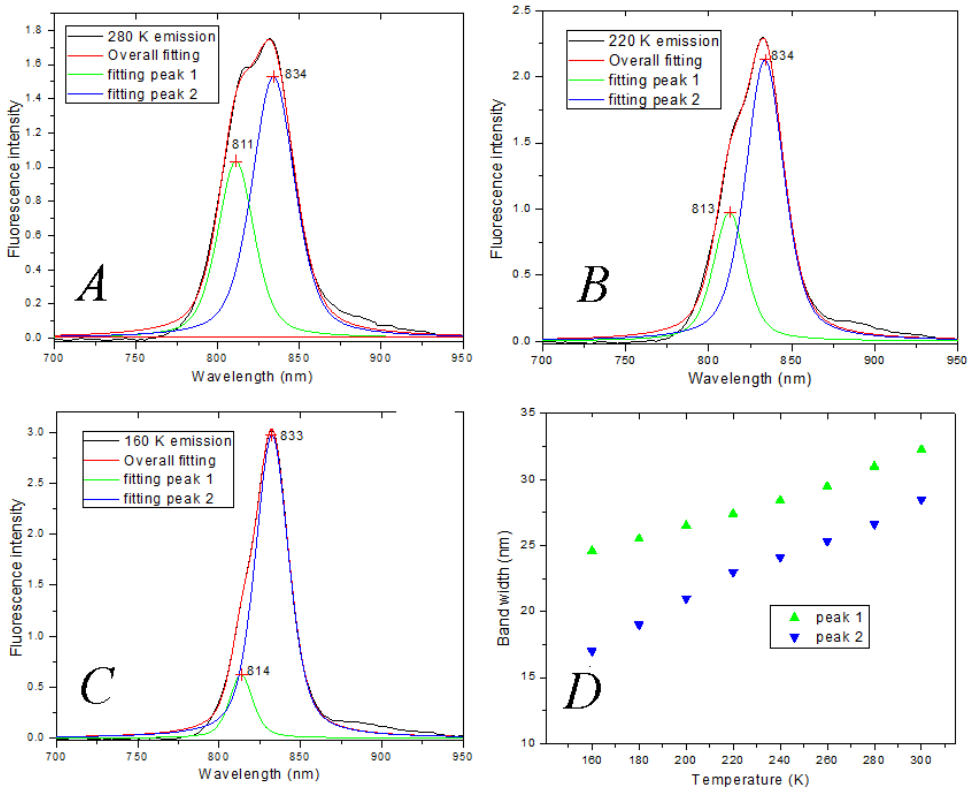
Jianzhong Wen[1,2], Yusuke Tsukatani[3], Weidong Cui[2], Hao Zhang[2], Michael L. Gross[2], Donald A. Bryant[3], Robert E. Blankenship[1,2]*



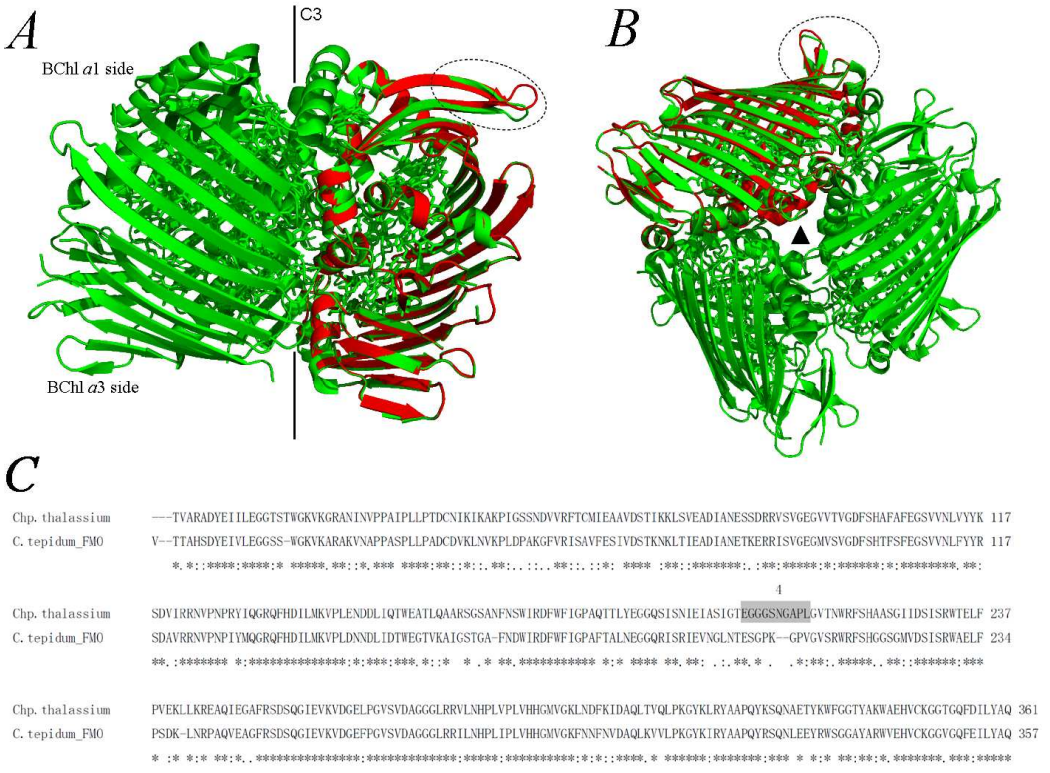
SI Fig. 1 Elution profiles of C. thermophilum FMO and protein standards from the analytical gel filtration column.



SI Fig. 2 Sequence alignment of the FMO protein from *Chlorobaculum tepdium* (C. tepidum_FMO) and *Candidatus* Chloroacidobacterium thermophilum (C.thermophilum_FMO) used for structure homology modeling. Six sequence insertion or deletion regions are labeled sequentially from 1 to 6, which show structural differences on the C. thermophilum FMO in comparison to FMO structure from *C. tepdium.*



SI Fig. 3 The fluorescence emission spectra of C. thermophilum FMO at 280 (*A*), 220 (*B*) and 160 K (*C*) were deconvoluted by two Gaussian-Lorentzian Sum function using PeakFit. The widths of the two deconvoluted peaks are plotted against the temperature in panel (*D*). A linear relationship between the peak widths and temperature exhibited.



SI Fig. 4 Homology structural modeling of the FMO protein from *Chp. thalassium*, which is the distantly related form of FMO in GSB. (*A*) Side view of the FMO trimer. (*B*) View of the FMO trimer from the BChl *a*3 side. Homology structure of the *Chp. thalassium* FMO protein (red) shows much more structural similarity to the FMO from *C. tepidum* (green) except the CsmA binding region, which is circled. The CsmA from *Chp. thalassium* is also quite divergent from the other CsmAs of GSB (main text). (*C*) Sequence alignment of FMOs from *Chp. thalassium* and *C. tepidum*. The structurally different region is highlighted and corresponding to region 4.